

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ryals, John
Delaney, Terry
Friedrich, Leslie
Weymann, Kristianna
Lawton, Kay
Ellis, Daniel
Uknes, Scott
Jesse, Taco
Vos, Pieter

(ii) TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESISTANCE IN PLANTS

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Novartis Corporation
(B) STREET: 520 White Plains Road, P.O. Box 2005
(C) CITY: Tarrytown
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10591

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meigs, J. Timothy
(B) REGISTRATION NUMBER: 38,241
(C) REFERENCE/DOCKET NUMBER: CGC 1909

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (919) 541-8587
(B) TELEFAX: (919) 541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20070920 55062001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCTTGAAGAT GAAAGCCAAA TAGAGAACCT CCAACATGAA ATCCACCGCC GGCCGGCAAG	3300
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GTATTCCGGT	ATTGGTCTTG	TATCATTATA	ACAAAGCAAT	ATCCCATGAC	GTGCATCACA	8700
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 2787..3347
 - (D) OTHER INFORMATION: /product= "1st exon of NIM1"
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 3427..4162
 - (D) OTHER INFORMATION: /product= "2nd exon of NIM1"
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 4271..4474
 - (D) OTHER INFORMATION: /product= "3rd exon of NIM1"
- (ix) FEATURE:
 - (A) NAME/KEY: exon
 - (B) LOCATION: 4586..4866
 - (D) OTHER INFORMATION: /product= "4th exon of NIM1"
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CGTCTACCAA AAACAGACAG ATTAATTTTT TCCAACCCGA TACAAGTTTC GGGGTTCTTG 360
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ATGCAGATTC CTCTCTCTTC TCAGTTTCCA GCAACATCGA GTCCGGAAAA CACCAATCAA	1860
GTGAAGGATG AGCCAAATTT GTTTAGACGT GTTATGAATT TGCTTTTACG TCGTAGTTAT	1920
TGAAAAAGCT GATTTATCGC ATGATTGAGA ACGAGAAGTT GAAGGCAAAT AACTAAAGAA	1980
GTCTTTTATA TGTATACAAT AATTGTTTTT AAATCAAATC CTAATTAAAA AAATATATTC	2040
ATTATGACTT TCATGTTTTT AATGTAATTT ATTCCTATAT CTATAATGAT TTTGTTGTGA	2100
AGAGCGTTTT CATTTGCTAT AGAACAAGGA GAATAGTTCC AGGAAATATT CGACTTGATT	2160
TAATTATAGT GTAAACATGC TGAACACTGA AAATTACTTT TTCAATAAAC GAAAAATATA	2220
ATATACATTA CAAAACCTAT GTGAATAAAG CATGAACTT AATATACGTT CCCTTTATCA	2280
TTTTACTTCA AAGAAAATAA ACAGAAATGT AACTTTCACA TGTAATCTA ATTCTTAAAT	2340

TTAAAAAATA ATATTTATAT ATTTATATGA AAATAACGAA CCGGATGAAA AATAAATTTT	2400
ATATATTTAT ATCATCTCCA AATCTAGTTT GGTCAGGGG CTTACCGAAC CGGATTGAAC	2460
TTCTCATATA CAAAAATTAG CAACACAAAA TGTCCTCCGT ATAAATACTA ACATTTATAA	2520
CCCGAACCGG TTTAGCTTCC TGTATATATCT TTTTAAAAAA GATCTCTGAC AAAGATTCCCT	2580
TTCTTGAAA TTTACCGGTT TTGGTGAAAT GTAAACCGTG GGACGAGGAT GCTTCTTCAT	2640
ATCTCACCAC CACTCTCGTT GACTTGACTT GGCTCTGCTC GTCAATGGTT ATCTTCGATC	2700
TTTAACCAAA TCCAGTTGAT AAGGTCTCTT CGTTGATTAG CAGAGATCTC TTTAATTTGT	2760
GAATTTCAAT TCATCGGAAC CTGTTG ATG GAC ACC ACC ATT GAT GGA TTC GCC	2813
Met Asp Thr Thr Ile Asp Gly Phe Ala	
1 5	
GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC GCT ACC GAT AAC ACC	2861
Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp Asn Thr	
10 15 20 25	
GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA GTA CTC ACC GGA CCT	2909
Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr Gly Pro	
30 35 40	
GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC TTC GAA TCC GTC TTT	2957
Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser Val Phe	
45 50 55	
GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG CTT GTT CTC TCC GAC	3005
Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu Ser Asp	
60 65 70	
GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG TCA GCG AGA AGC TCT	3053
Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser	
75 80 85	
TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG GAG AAA GAC TCC AAC	3101
Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp Ser Asn	
90 95 100 105	
AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT GCC AAG GAT TAC	3149
Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys Asp Tyr	
110 115 120	
GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC	3197
Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser	
125 130 135	
AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG	3245
Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu	
140 145 150	
AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG	3293
Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu	
155 160 165	
GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC	3341
Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu	
170 175 180 185	
TAT CAG GTAAACACC ATCTGCATTA AGCTATGGTT ACACATTCAT GAATATGTTC	3397
Tyr Gln	

TTACTTGAGT	ACTTGTATTT	GTATTTTCAG	AGG	CAC	TTA	TTG	GAC	GTT	GTA	GAC	3450
			Arg	His	Leu	Leu	Asp	Val	Val	Asp	190
AAA	GTT	GTT	ATA	GAG	GAC	ACA	TTG	GTT	ATA	CTC	3498
Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	200
											205
TGT	GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	GAT	AGA	3546
Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	215
											220
GTC	AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	CTT	GAA	3594
Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	230
											235
GAG	CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	CGT	AAA	3642
Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	245
											250
GTA	CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	AAT	GTA	3690
Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	260
											265
TCG	GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	CTT	TTG	3738
Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	280
											285
AAT	CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT	TTC	GCT	3786
Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	295
											300
GTG	AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA	CTT	GAT	3834
Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	310
											315
CAT	AGG	AAT	CCG	AGG	GGA	TAT	ACG	GTG	CTT	CAT	3882
His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	325
											330
AAG	GAG	CCA	CAA	TTG	ATA	CTA	TCT	CTA	TTG	GAA	3930
Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	340
											345
TCA	GAA	GCA	ACT	TTG	GAA	GGT	AGA	ACC	GCA	CTC	3978
Ser	Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	Ala	Leu	350
											365
GCC	ACT	ATG	GCG	GTT	GAA	TGT	AAT	AAT	ATC	CCG	4026
Ala	Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	Ile	Pro	375
											380
TCT	CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA	ATA	CTA	4074
Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	390
											395
CGA	GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT	CCC	TCT	4122
Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	405
											410
GAT	GAA	TTG	AAG	ATG	ACG	CTG	CTC	GAT	CTT	GAA	4162
Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	420
											425
											430

GTATCTATCA AGTCTTATTT CTTATATGTT TGAATTAAAT TTATGTCCTC TCTATTAGGA	4222
AACTGAGTGA ACTAATGATA ACTATTCTTT GTGTCGTCCA CTGTTTAG TT GCA CTT Val Ala Leu 435	4278
GCT CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala 440 445 450	4326
GAA ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp 455 460 465	4374
CGT CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro 470 475 480	4422
TTC AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys 485 490 495	4470
ACC G GTATGGATTC TCACCCACTT CATCGGACTC CTTATCACAA AAAACAAAAC Thr 500	4524
TAAATGATCT TTAAACATGG TTTTGTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA	4584
G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu 505 510 515	4629
GAC CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu 520 525 530	4677
GAC GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu 535 540 545	4725
ATA CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu 550 555 560	4773
GGA AAT TCG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr 565 570 575	4821
GGT GGA AAG AGG TCT AAC CGT AAA CTC TCT CAT CGT CGT CGG TGA Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg Arg * 580 585 590	4866
GACTCTTGCC TCTTAGTGTA ATTTTGTCTG TACCATATAA TTCTGTTTTT ATGATGACTG	4926
TAACTGTTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTTCGTTTTG CATCCTGTGT	4986
ATTATTGCTG CAGGTGTGCT TCAAACAAAT GTTGTAACAA TTTGAACCAA TGGTATACAG	5046
ATTTGTAATA TATATTTATG TACATCAACA ATAACCCATG ATGGTGTTAC AGAGTTGCTA	5106
GAATCAAAGT GTGAAATAAT GTCAAATTGT TCATCTGTTG GATATTTTCC ACCAAGAACC	5166
AAAAGAATAT TCAAGTTCCC TGAAGTTCTG GCAACATTCA TGTTATATGT ATCTTCCTAA	5226
TTCTTCCTTT AACCTTTTGT AACTCGAATT ACACAGCAAG TTAGTTTCAG GTCTAGAGAT	5286

Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys
210 215 220

Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser
225 230 235 240

Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu
245 250 255

Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys
260 265 270

Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu
275 280 285

Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala
290 295 300

Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala
305 310 315 320

Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala
325 330 335

Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly
340 345 350

Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
355 360 365

Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln
370 375 380

Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
385 390 395 400

Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala
405 410 415

Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
420 425 430

Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met
435 440 445

Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu
450 455 460

Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys
465 470 475 480

Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala
485 490 495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser
500 505 510

Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala
515 520 525

Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg
530 535 540

Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1           5           10           15

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
          20           25           30

Val His Tyr Ala Val Gln His Cys Asn
          35           40

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val
1           5           10           15

Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln
          20           25

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1           5           10           15

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
          20           25           30

Val His Tyr Ala Val Gln His Cys Asn
          35           40

```

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val
 1 5 10 15
 Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
 1 5 10 15
 Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
 20 25 30
 Val His Tyr Ala Val Gln His Cys Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro
 1 5 10 15
 Asp Met Val

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTCTAAAG CATGCCGATC GG

22

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATCCGATC GGCATGCTTT A

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTCTAAAC CATGGCGATC GG

22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

AATTCCGATC GCCATGGTTT A

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCAGCTGGAA TTCCG

15

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGAATTCCA GCTGGCATG

19

10079035.021902
"SEQ ID NO:16"